

STIC-Biotech/ChemLib

102555

From: Chen, Shin-Lin
Sent: Wednesday, August 27, 2003 7:17 PM
To: STIC-Biotech/ChemLib
Subject: sequence search: 09/865,018

Please perform the following **sequence search** for Application No. **09/865,018** ASAP. Thanks!

SEQ ID NOs. 1 and 2.

Shin-Lin Chen
AU 1632
CM1 12A15
Mail Box: CM1 12E12
(703) 305-1678

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____





STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number

TO: Shin-Lin Chen
Location: CM1/12A15/12E12
Art Unit: 1632
Tuesday, September 02, 2003

Case Serial Number: 09865018

From: Mary Jane Ruhl
Location: Biotech-Chem Library
CM1-6A06
Phone: 605-1155

maryjane.ruhl@uspto.gov

Search Notes

Examiner Chen,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
CM-1, Rm. 6-A-06
605-1155

11

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 29, 2003, 15:25:11, Search time 2600 seconds

(without alignments)
938480 Million cell updates/sec

Title: US-09-865-018B-1

Perfect score: 597

Sequence: 1 atgtcaaaagtgtgagtgatgc

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 577422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Listing first 45 summaries

```

GenBank: *
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2: gb_htg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
7: gb_ph:*
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34: em_htg_mus:*
35: em_htg_pln:*
36: em_htg_rtd:*
37: em_htg_rtm:*
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40: em_htg_mus:*
41: em_htg_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597	100.0	597	AR000109	AR000109 Sequence
2	597	100.0	597	AR125445	AR125445 Sequence
3	597	100.0	597	AR157684	AR157684 Sequence
4	597	100.0	597	AR219459	AR219459 Sequence
5	597	100.0	597	AR282523	AR282523 Sequence
6	597	100.0	597	AR282516	AR282516 Sequence
7	597	100.0	597	AR282515	AR282515 Sequence
8	597	100.0	597	AR282514	AR282514 Sequence
9	595.4	99.7	234	AR247551	AR247551 Homo sapi
10	595.4	99.7	234	AR247551	AR247551 Homo sapi
11	592.8	97.5	230	AR282515	AR282515 Homo sapi
12	593.4	99.4	1098	AR219451	AR219451 Sequence
13	593.4	99.4	1098	AR282515	AR282515 Sequence
14	593.4	99.4	1098	AR282515	AR282515 Sequence
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31	518.6	86.9	1327	AR011957	AR011957 Sus scrofa
32	518.6	86.9	1301	AR011956	AR011956 Sus scrofa
33	518.6	86.9	1301	AR011955	AR011955 Sus scrofa
34	518.6	86.9	1301	AR011954	AR011954 Sus scrofa
35	499.4	83.7	557	AR219452	AR219452 Sequence
36	499.4	83.7	557	AR262152	AR262152 Sequence
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44	498.4	83.5	1028	AR282518	AR282518 Sequence
45	498.4	83.5	1028	AR282518	AR282518 Sequence

ALIGNMENTS

RESULT 1	AR000109	597 bp	DNA	Linear	PA1 04-03-1998
LOCUS	AR000109	Sequence	from patent US 5736418		
DEFINITION	AR000109	Sequence	from patent US 5736418		
ACCESSION	AR000109	Sequence	from patent US 5736418		
VERSION	AR000109.1	GI:5962640			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 597)				
AUTHORS	Munger K. and Jones D. Leanne.				
TITLE	Method and kit for evaluating human papillomavirus trans. and cells				
JOURNAL	Patent: US 5736418-A 3 07-APR-1998				

[illegible][illegible]

Db 241 AAGGCGAGCTTGGCCAGTTCTACATACAGACCTTGGGAGCTTTAAAGAGCTTGGGAG 400
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 Db 301 GTGCGGAGCTTGGAGAGAGTAAATATATTAAGAGAGTATATATATATATATATATATAT 360
 QY 361 GTGCGGAGCTTGGAGAGAGTAAATATATTAAGAGAGTATATATATATATATATATATAT 420
 Db 361 GTGCGGAGCTTGGAGAGAGTAAATATATTAAGAGAGTATATATATATATATATATATAT 420
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 Db 421 CAGACGGGGTTAGCGGAGCAATGCGGAGGATATAGAGAGAGTATATATATATATATATATAT 480
 QY 481 TCTACTCAAAACAAAGAGCCAGACAGACAGAGAAATATATATATATATATATATATAT 540
 Db 481 TCTACTCAAAACAAAGAGCCAGACAGACAGAGAAATATATATATATATATATATATAT 540
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 Db 541 GCGCGGTTCTGTGAGAGAGAGCGGCGGAGAGAGCTTGTCTAGAGAGAGCTTAAAGCTAA 597
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 HSU10906 597 bp mRNA linear PFI 27-Jul-1994
 LOCUS Human cyclin-dependent kinase inhibitor p27kip1 mRNA, complete cds.
 DEFINITION
 ACCESSION U10906.1 GI:516558
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catartida; Homnidae; Homo.
 1 (bases 1 to 597)
 Poljak, R., Lee, M., Hong, J., Erdjument-Bromage, H., Koff, A., Roberts, J. M., Tempst, P., and Massague, J.
 Cloning of p27kip1, a cyclin-dependent kinase inhibitor, and a potential mediator of extracellular antimitogenic signals
 Cell 78, 56-66 (1994)
 2 (bases 1 to 597)
 Massague, J.
 Direct Submission
 Submitted (15-JUN-1994) M -R Lee and J Massague, Cell Biology and Genetics, Memorial Sloan-Kettering Cancer Center, 1275 York Avenue, New York, NY 10021, USA
 JOURNAL
 AUTHORS
 TITLE
 FEATURES
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 BASE COUNT 161 a 164 c 185 g 87 t
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 Query Match 100.0% Score 597; DR 9; Length 597;
 Best Local Similarity 100.0%; Pred. No. 3,1e-133;
 Matches 597; Conservative 0; Mismatches 0; Indels 0; Gap 0
 QY 1 ATCTCAAGCTGGAATGCTACTACGAGGAGGCTTATCTGAGAGGATATGAGAGCTTAAAGCTAA 60

Db 1 ATCTCAAGCTGGAATGCTACTACGAGGAGGCTTATCTGAGAGGATATGAGAGCTTAAAGCTAA 60
 QY 61 GTGAGAGCTGCGGAGAGCTGCGGAGAGAGCTTGTGCGGCTGCGGAGAGAGAGAGAGAGAG 120
 Db 61 GTGAGAGCTGCGGAGAGCTGCGGAGAGAGCTTGTGCGGCTGCGGAGAGAGAGAGAGAGAG 120
 QY 121 TTAACCGCGGAGCTTGGAG 180
 Db 121 TTAACCGCGGAGCTTGGAG 180
 QY 181 AATTTCGATTTTTCATATATCAATCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 Db 181 AATTTCGATTTTTCATATATCAATCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 QY 241 AAGGAGAGCTTGTGAG 300
 Db 241 AAGGAGAGCTTGTGAG 300
 QY 301 GTGCGGAGCTTGGAG 360
 Db 301 GTGCGGAGCTTGGAG 360
 QY 361 GTGCGGAGCTTGGAG 420
 Db 361 GTGCGGAGCTTGGAG 420
 QY 421 CAGACGGGGTTAGCGGAGCAATGCGGAGGATATAGAGAGAGTATATATATATATATATATAT 480
 Db 421 CAGACGGGGTTAGCGGAGCAATGCGGAGGATATAGAGAGAGTATATATATATATATATATAT 480
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 Db 481 TCTACTCAAAACAAAGAGCCAGACAGACAGAGAAATATATATATATATATATATATAT 540
 QY 541 GCGCGGTTCTGTGAGAGAGAGCGGCGGAGAGAGCTTGTCTAGAGAGAGCTTAAAGCTAA 597
 Db 541 GCGCGGTTCTGTGAGAGAGAGCGGCGGAGAGAGCTTGTCTAGAGAGAGCTTAAAGCTAA 597
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 AF247551 597 bp mRNA linear PFI 11 MAY 2000
 LOCUS Homo sapiens cyclin-dependent kinase inhibitor p27kip1 mRNA, complete cds.
 DEFINITION
 ACCESSION AF247551.1 GI:7769664
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catartida; Homnidae; Homo.
 1 (bases 1 to 597)
 Wang, W.-L., Yang, X.-K., and Yu, X.-X.
 Homo sapiens cyclin-dependent kinase inhibitor p27kip1 cDNA
 Unpublished
 2 (bases 1 to 597)
 Li, J., Wang, W.-L., Yang, X.-K., and Yu, X.-X.
 Direct Submission
 Submitted (20 MAY 2000) Department, Fourth Military Medical University, No. 17 Changle West Rd., Xi'an, Shaanxi 710042, P. R. China
 JOURNAL
 AUTHORS
 TITLE
 FEATURES
 source
 1..597
 /organism="Homo sapiens"
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 /db_xref="GI:7769665"

[illegible]



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 29, 2003, 15:25:16 Search time 248 seconds

(Without alignments)
6498,244 Million cell -data/seq

Title: US-09-865-018b-1

Perfect score: 1 atgtcaaacgtgcagatgttc tccagagacttcaaacgtaa 597

Scoring table: IDENTITY_NUC

Gapop 10 0 , Gapext 1 0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DR seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the full score distribution, and is derived by analysis of the full score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description
1	597	100.0	597	19	AAV47517	CDNA encoding prot
2	597	100.0	597	19	AAV16719	Nucleotide sequence
3	597	100.0	597	20	AAV21917	CR177P protein p2
4	597	100.0	597	21	AAV30920	Human p27 protein
5	597	100.0	597	21	AAV40494	Human cyclin depen
6	597	100.0	597	21	AAV50519	Human cyclin depen
7	597	100.0	597	21	AAV29564	Human p27(Kip1) N1
8	597	100.0	597	22	AAV28328	Nucleotide sequence

9	597	100.0	597	22	AAV91621	Human p27 protein
10	597	100.0	597	24	AAV79025	Hypoxia-inducible p27-Kip1 cDNA, full
11	597	100.0	597	24	AAV72896	Human p27 Kip1 cDN
12	596	99.8	596	17	AAV16386	CDK inhibitor p27
13	593.4	99.4	1098	18	AAV74054	Human p16p27
14	593.4	99.4	1098	20	AAV26224	Human p16p27
15	593.4	99.4	1098	20	AAV90926	Human Wt protein c
16	593.4	99.4	1098	21	AAV50451	CDNA encoding p16 p
17	593.4	99.4	1098	21	AAV50526	CDNA encoding p16 p
18	593.4	99.4	1098	21	AAV21052	CDNA encoding p16 p
19	593.4	99.4	1143	20	AAV24222	Human p16p27
20	593.4	99.4	1143	21	AAV90925	Human Wt protein c
21	593.4	99.4	1143	21	AAV50490	CDNA encoding p16 p
22	593.4	99.4	1143	21	AAV50525	CDNA encoding p16 p
23	592.2	99.2	597	21	AAV51357	Human p27 Kip1
24	591	99.0	1420	18	AAV174051	CDK inhibitor p27
25	591	99.0	1420	20	AAV26220	Human p16p27
26	591	99.0	1420	20	AAV90922	Human Wt protein c
27	591	99.0	1420	21	AAV50486	CDNA encoding p27 p
28	591	99.0	1420	21	AAV50523	CDNA encoding p27 p
29	589.4	98.7	1121	20	AAV50525	Human p16p27
30	587.8	98.5	1121	21	AAV90924	Human p16p27
31	587.8	98.5	1121	21	AAV50189	CDNA encoding p27 p
32	587.8	98.5	1121	21	AAV50524	CDNA encoding p27 p
33	582	97.5	582	20	AAV17252	CDNA encoding p27 p
34	518.6	85.9	1958	24	AAV01080	Human p27 Kip1
35	499.4	84.7	557	20	AAV26229	Human p27 Kip1
36	499.4	84.7	557	21	AAV90927	Human p27 Kip1
37	499.4	84.7	557	21	AAV50492	Human p27 Kip1
38	499.4	84.7	557	21	AAV50527	Human p27 Kip1
39	498.6	84.5	1928	20	AAV24231	Human p16p27
40	498.6	84.5	1928	21	AAV90929	Human Wt protein c
41	498.6	84.5	1928	21	AAV50194	CDNA encoding p16 p
42	498.6	84.5	1928	21	AAV50529	CDNA encoding p16 p
43	498.4	84.5	1973	26	AAV24232	Human p16p27
44	498.4	84.5	1973	26	AAV90928	Human Wt protein c
45	498.4	84.5	1973	21	AAV50493	CDNA encoding p16 p

ALIGNMENTS

RESULT 1
ID AAV47517 standard: cDNA: 597 bp.

AC AAV47517:
27-OCT-1998 (first entry)

CDNA encoding protein inhibiting activation of cyclin E-Cdk2 complex.
27-MAR-1998, 17, Kip1, inhibits activation of cyclin E-Cdk2 complex.
CDNA encoding p27 Kip1, dependent kinase complex by cell proliferative disease.
recurrence treatment, human; ss.

XX Homo sapiens.

XX 1-597
XX 1-597

XX 1-597
XX 1-597

XX 1-597
XX 1-597

XX 1-597
XX 1-597

XX 1-597
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XX 1-597
XX 1-597

XX 1-597
XX 1-597

QY 181 AATTGCAATTTTCAGAAATCAAAATCTTACAGGCTTAAGTCACTGCTTAAAGACTTGTAG 240
 CC |||||||
 CC disorder. The methods are useful for diagnosing disorders associated with
 CC hyperproliferation, evaluating their aggressiveness and/or rate of
 CC recurrence and as prognosis for evaluating a cancer patient's risk of
 CC death. From the observations, treatment can be applied on the basis of
 CC the patient's risk of death and/or recurrence of the cancer. The
 CC diagnostic methods may also be employed as follow-up to treatment,
 CC e.g. quantitation of the level of p27 protein may be indicative of the
 CC effectiveness of current or previously employed cancer therapies as well
 CC as the effect of these therapies upon patient prognosis. The methods and
 CC reagents allow the detection of loss of p27 protein from a cell in order
 CC to diagnose and phenotype proliferative disorders arising from
 CC tumorigenic transformation of cells, or other hyperplastic or neoplastic
 CC transformation processes as well as degenerative disorders such as
 CC degeneration of tissue e.g. neurodegeneration.
 CC XX
 Db 421 CAGAGCGGCTTAACTAGGAGCTAAATGCTCAAGAAATAGGAGAGAGAGAGAGAGAGAGAG 480
 CC |||||||
 QY 481 TCTACTCAAAACAAAAGAGGCTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 CC |||||||
 Db 481 TCTACTCAAAACAAAAGAGGCTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 CC |||||||
 QY 541 GCGGCTTCTGTGAG 597
 CC |||||||
 Db 541 GCGGCTTCTGTGAG 597
 CC |||||||

RESULT 3

AAX21817
 ID AAX21817 standard: cDNA: 597 BP.

XX AAX21817:

XX 14-MAY-1999 (first entry)

DE CK1/KIP protein p27 coding sequence.

KM CK1/KIP protein; p27 protein, cyclin kinase inhibitor, cancer;
 hyperproliferative disorder; ds.

OS Homo sapiens.

PN W09904238-A2.

PD 28-JAN-1999.

PF 14-JUL-1998; 98WO-US14566.

PR 15-JUL-1997; 97US-0893276.

PA (DEAC-) DEACONESS HOSPITAL.

PI (MITO-) MITOTIX INC.

PI Draetta G, Loda M, Pagano M, Rolfe M;

DR WPL: 1999-132426/11.

DR P-PSDB: AAY00768.

PT Methods for diagnosis and prognosis of hyperproliferative disorders
 PT - by determining the level of cyclin kinase inhibitor protein(s),
 PT particularly p27

PS Claim 19; Page 36-37; 53pp; English.

CC This sequence encodes the cyclin kinase inhibitor (CKI) protein p27. The
 CC invention relates to a method for diagnosing a hyperproliferative
 CC disorder, associated with the destabilisation of a CKI protein in cells
 CC of a patient, comprises: (i) ascertaining the CKI protein level in a
 CC sample of patient cells; and (ii) diagnosing the presence or absence of a
 CC hyperproliferative disorder by utilising the ascertained CKI protein
 CC level, where a reduced CKI protein level, relative to a normal control

CC cell sample, correlates with the presence of a hyperproliferative
 CC disorder. The methods are useful for diagnosing disorders associated with
 CC hyperproliferation, evaluating their aggressiveness and/or rate of
 CC recurrence and as prognosis for evaluating a cancer patient's risk of
 CC death. From the observations, treatment can be applied on the basis of
 CC the patient's risk of death and/or recurrence of the cancer. The
 CC diagnostic methods may also be employed as follow-up to treatment,
 CC e.g. quantitation of the level of p27 protein may be indicative of the
 CC effectiveness of current or previously employed cancer therapies as well
 CC as the effect of these therapies upon patient prognosis. The methods and
 CC reagents allow the detection of loss of p27 protein from a cell in order
 CC to diagnose and phenotype proliferative disorders arising from
 CC tumorigenic transformation of cells, or other hyperplastic or neoplastic
 CC transformation processes as well as degenerative disorders such as
 CC degeneration of tissue e.g. neurodegeneration.
 CC XX

Query Match 100.0%; Score 597; DB 20; Length 597;

Best Local Similarity 100.0%; Pred. No. E-9e-160;

Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCTAAATGCTGAG 60

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1 ATGCTAAATGCTGAG 60

1 ATGCTAAATGCTGAG 60

1 ATGCTAAATGCTGAG 60

1 ATGCTAAATGCTGAG 60

1 ATGCTAAATGCTGAG 60

GenCore Version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: August 29, 2003, 16:07:16 (Search time 62 Seconds)

(without alignments)
4250 092 Million cell updates/sec

Title: US-09-865-018B-1

Perfect score: 597

Sequence: 1 atgtcaaacgtgcgagtc

ttcgaagagctcgaagttaa 597

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 56978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 115956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Issued_Patents_NA*

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2: /cgnt2_6/ptodata/2/1na/5b.COMB.seq.*
3: /cgnt2_6/ptodata/2/1na/6a.COMB.seq.*
4: /cgnt2_6/ptodata/2/1na/6b.COMB.seq.*
5: /cgnt2_6/ptodata/2/1na/ptnns.COMB.seq.*
6: /cgnt2_6/ptodata/2/1na/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	597	100.0	597	US-08-406-248-3	Sequence 1, Appl
2	597	100.0	597	US-08-897-333A-1	Sequence 1, Appl
3	597	100.0	597	US-08-240-606-6	Sequence 5, Appl
4	597	100.0	597	US-08-794-002-1	Sequence 1, Appl
5	597	100.0	597	US-09-457-568-25	Sequence 25, Appl
6	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
7	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
8	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
9	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
10	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
11	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
12	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
13	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
14	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
15	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
16	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
17	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
18	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
19	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
20	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
21	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
22	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
23	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
24	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
25	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
26	597	100.0	597	US-09-457-646-25	Sequence 25, Appl
27	597	100.0	597	US-09-457-646-25	Sequence 25, Appl

28	499.4	83.7	557	US-09-516-065-11	Sequence 11, Appl
29	496.0	83.5	1028	US-09-457-646-25	Sequence 15, Appl
30	496.5	83.5	1928	US-09-457-646-15	Sequence 15, Appl
31	498.6	83.5	1028	US-08-902-572-21	Sequence 21, Appl
32	498.6	83.5	1028	US-09-516-065-15	Sequence 15, Appl
33	498.4	83.5	1073	US-09-457-646-13	Sequence 13, Appl
34	498.4	83.5	1073	US-09-457-646-13	Sequence 13, Appl
35	498.4	83.5	1073	US-08-902-572-23	Sequence 23, Appl
36	498.4	83.5	1073	US-09-516-065-13	Sequence 13, Appl
37	467.6	78.3	594	US-08-854-0396-7	Sequence 7, Appl
38	467.6	78.3	594	US-09-240-906-7	Sequence 7, Appl
39	467.6	78.3	594	US-08-794-002-3	Sequence 3, Appl
40	447.6	75.0	534	US-08-854-0396-5	Sequence 5, Appl
41	447.6	75.0	534	US-09-457-646-29	Sequence 29, Appl
42	213.2	35.7	922	US-09-516-065-29	Sequence 29, Appl
43	213.2	35.7	922	US-09-457-646-21	Sequence 21, Appl
44	212.6	35.6	782	US-09-457-646-21	Sequence 21, Appl
45	212.6	35.6	782	US-09-457-646-21	Sequence 21, Appl

ATTACHMENTS

RESULT 1
US-08-406-248-3
Sequence 3, Application US/08406248
Patent No. 5736318
GENERAL INFORMATION:
APPLICANT: Munger, Karl
TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc., 901 N. Zeeb Rd., P.O. Box 1617, Littleton, CO 80120
CITY: Littleton
STATE: CO
COUNTRY: USA
ZIP: 80120
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
AFFIDAVIT No. 248
CLASSIFICATION: 406
ATTORNEY/AGENT INFORMATION:
NAME: MUNGER, KARL
REGISTERED NUMBER: 00194
REFERENCE TO OTHER NUMBERS: 00194
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ. ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Adult
TISSUE TYPE: Kidney
IMMEDIATE SOURCE:
CLONE: p27k1p1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..597
PUBLICATION INFORMATION:


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1 PRIOR APPLICATION NUMBER: 60/128,518
2 PRIOR FILING DATE: 1999-04-09
3 PRIOR APPLICATION NUMBER: 60/128,271
4 PRIOR FILING DATE: 1999-04-08
5 PRIOR APPLICATION NUMBER: 60/122,974
6 PRIOR FILING DATE: 1999-03-01
7 NUMBER OF SEQ. ID NOS.: 32
8
9 SOFTWARE: PatentIn Ver. 2.0
10
11 SEQ. ID NO. 25
12
13 LENGTH: 597
14
15 TYPE: DNA
16
17 ORGANISM: Homo sapiens
18
19 US-09-516-065-25

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Query Match	100.0%	Score 597;	DB 4;	Length 597;
Best Local Similarity	100.0%;	Prod. No	2 6- 170.	
Matches 597; Conservative	0;	Mismatches	0;	Indels 0;

[illegible]

RESULT 8 -
US-09-457-568-9
Sequence 9, Application US/09457568
Patent No. 641943
GENERAL INFORMATION:
APPLICANT: McArthur, James G
APPLICANT: Gyulalis, Jeno
TITLE OF INVENTION: Method and Apparatus for
TITLE OF INVENTION: Smooth Muscle Cells
FILE REFERENCE: 106482, 691
CURRENT APPLICATION NUMBER: US/09/457, 568
CURRENT FILING DATE: 1999-12-09
EARLIER APPLICATION NUMBER: 60/1122, 974

1 EARLIER FILING DATE: 1946-03-01
2
3 EARLIER APPLICATION NUMBER: 65240
4
5 EARLIER FILING DATE: 1999-11-05
6
7 NUMBER OF SEQ ID NOS: 28
8
9 SOFTWARE: Patented Ver. 2.0
10
11 SEQ ID NO 9
12
13 LENGTH: 1098
14
15 TYPE: DNA
16
17 ORGANISM: Homo sapiens
18
19 US-05-457-566-9

Query Match	99.48;	Score 593.4;	DB 4;	Length 1098;
Best local Similarity	99.88;	Pred. No. 4.3e-169;		
Matches 594;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

[illegible]

1 RESUMÉ 9
 2 US-09-457-646-9
 3 Sequence 9, Application US/09457646
 4 Patent No. 6420345
 5 GENERAL INFORMATION:
 6 APPLICANT: Patel, Sallil D
 7 APPLICANT: McArthur, James G
 8 APPLICANT: Gyuris, Jero
 9 TITLE OF INVENTION: Methods and Reagents for
 10 Inhibiting Proliferation of
 11 LILIE OF INVENTION: R. Smooth Muscle Cells
 12 FILE REFERENCE: 106482, 287
 13 PCT NO. APL/CAI: P. H. 28648, US, 07, 457, 646
 14 CURRENT FILING DATE: 1999-12-09
 15 EARLIER APPLICATION H. 28648, 09, 129, 974
 16 EARLIER FILING DATE: 1999-03-01
 17 EARLIER APPLICATION H. 28648, 60/16, 682
 18 EARLIER FILING DATE: 1999-11-05


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: Sequence 5, Application US/0951665
: Patent No. 6521602
: GENERAL INFORMATION:
: APPLICANT: Patel, Sallil D
: APPLICANT: McArthur, James G
: APPLICANT: Gyuris, Jeno
: APPLICANT: Mendez, Michel
: APPLICANT: Finer, Mitchell
: TITLE OF INVENTION: Anti-Neoplastic Compositions and Uses thereof
: FILE REFERENCE: Col: 406; 106482.692
: CURRENT APPLICATION NUMBER: US/09/516.065
: PRIORITY FILING DATE: 2000-03-01
: PRIOR APPLICATION NUMBER: 60/128.515
: PRIORITY FILING DATE: 1999-04-09
: PRIOR APPLICATION NUMBER: 60/128.271
: PRIORITY FILING DATE: 1999-04-08
: PRIOR APPLICATION NUMBER: 60/122.974
: PRIORITY FILING DATE: 1999-03-01
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO: 9
: LENGTH: 1098
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-516-065-9

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Query Match      99.4%: Score 593.4: DB 4: Length 1098:
Best Local Similarity 99.8%: Pctd No. 4.4e-169:
Matches 594: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

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DB 504 GTCAACGTCAGTCTCTTAACGGAGCCCTAGCCTGAGCGGATGATGAGTAAAGG 563
OY 63 GGAAGTACCTTAAAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 122
DB 564 GGAAGTACCTTAAAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 523
OY 123 AATCGGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 182
DB 624 AATCGGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 683
OY 183 TTTCGATTTTCAATATCAAAATTTTCAATATTTTCAATATTTTCAATATTTT 242
DB 684 TTTCGATTTTCAATATCAAAATTTTCAATATTTTCAATATTTTCAATATTTT 743
OY 243 GGGTAACTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 402
DB 744 GGGTAACTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 803
OY 303 GCGGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 462
DB 804 GCGGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 863
OY 363 TTTCGATTTTCAATATCAAAATTTTCAATATTTTCAATATTTTCAATATTTT 422
DB 864 TTTCGATTTTCAATATCAAAATTTTCAATATTTTCAATATTTTCAATATTTT 923
OY 423 GATGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 482
DB 924 GATGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 983
OY 483 TACTCAAAACAAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 542
DB 984 TACTCAAAACAAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1043
OY 543 CGGTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 597
DB 1044 CGGTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1098

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RESULT 12
US-09-457-568-7

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: Sequence 7, Application US/9457568
: Patent No. 6418943
: GENERAL INFORMATION:
: APPLICANT: McArthur, James G
: APPLICANT: Gyuris, Jeno
: APPLICANT: Finer, Mitchell H
: TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
: FILE REFERENCE: 106482.691
: CURRENT APPLICATION NUMBER: 60/122.974
: PRIORITY FILING DATE: 1999-03-01
: PRIOR APPLICATION NUMBER: 60/122.974
: PRIORITY FILING DATE: 1999-11-05
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO: 7
: LENGTH: 1143
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-457-568-7

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Query Match      99.4%: Score 594.4: DB 4: Length 1143:
Best Local Similarity 99.8%: Pctd No. 4.4e-169:
Matches 594: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

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DB 546 GTCAACGTCAGTCTCTTAACGGAGCCCTAGCCTGAGCGGATGATGAGTAAAGG 608
OY 63 GGAAGTACCTTAAAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 122
DB 609 GGAAGTACCTTAAAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 668
OY 123 AATCGGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 182
DB 669 AATCGGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 728
OY 183 TTTCGATTTTCAATATCAAAATTTTCAATATTTTCAATATTTTCAATATTTT 242
DB 729 TTTCGATTTTCAATATCAAAATTTTCAATATTTTCAATATTTTCAATATTTT 788
OY 243 GGGTAACTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 402
DB 789 GGGTAACTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 848
OY 303 GCGGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 462
DB 849 GCGGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 908
OY 363 TTTCGATTTTCAATATCAAAATTTTCAATATTTTCAATATTTTCAATATTTT 422
DB 909 TTTCGATTTTCAATATCAAAATTTTCAATATTTTCAATATTTTCAATATTTT 968
OY 423 GATGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 482
DB 969 GATGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 1028
OY 483 TACTCAAAACAAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 542
DB 1029 TACTCAAAACAAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1088
OY 543 CGGTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 597
DB 1089 CGGTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1143

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RESULT 13
US-09-457-646-7
: Sequence 7, Application US/9457568
: Patent No. 6420345
: GENERAL INFORMATION:



RESULT 4
US-09-865-018-1
; Sequence 1, Application US/09865018
; Patent No. US2002011086A;
; GENERAL INFORMATION:

LID 0100000002ACASAOZAAIAAIGICAMTGGAGGOCOC GGNNOOCCGCCTTA


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; INFORMATION FOR SEQ ID NO: 17:
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; SEQUENCE CHARACTERISTICS:
;
;     LENGTH: 557 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;
;     MOLECULE TYPE: DNA
;
US-08-902-572-17

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Query Match	83.78	Score 499.4	IP 8	Length 557
Best Local Similarity	99.88	Pred. No. 1.2e-144		
Matches 500; Conservative	0	Mismatches 1	Indels 0	Gaps 0

[illegible]

RESULT 7
 US-08-902-572-21
 : Sequence 21 Application US/08902572
 : Publication No. US20020068706A1
 : GENERAL INFORMATION:
 : APPLICANT: Gyuris, Jeno
 : APPLICANT: Lamphere, Lou
 : APPLICANT: Beach, David H.
 : TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
 : TITLE OF INVENTION: RELATED THEREOF
 : NUMBER OF SEQUENCES: 34
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: FOLEY, HOAG & ELLIOT LLP
 : STREET One Post Office Square
 : CITY: Boston
 : STATE: MA
 : COUNTRY: USA
 : ZIP: 02109-2170
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.30

1 CURRENT APPLICATION DATA:
 2 APPLICATION NUMBER: US-06/7902,572
 3 FILING DATE: 28-JUL-1997
 4 CLASSIFICATION: 514
 5 ATTORNEY/AGENT INFORMATION:
 6 NAME: Vincent, Matthew P.
 7 REGISTRATION NUMBER: 35,709
 8 REFERENCE TO EXISTING APPLICATION: MTV-066, 044
 9 TELECOMMUNICATION INFORMATION:
 10 TELEPHONE: 617-832-1000
 11 TELEFAX: 617-832-7000
 12 INFORMATION FOR SEQ. ID NO.: 21:
 13 SEQUENCE CHARACTERISTICS:
 14 LENGTH: 1028 base pairs
 15 TYPE: nucleic acid
 16 STRANDEDNESS: single
 17 TOPOLOGY: linear
 18 MOLECULE TYPE: RNA
 19 US-08-902-572-21

Query Match	Score	DB #	Length
Best Local Similarity	98.28	Prod. No. 270-14	1028

[illegible]

RESULT 8
US-08-090-572-23
SEQUENCE 23, APPLICATION 98-08902572
PUBLICATION NO US20020608706A1
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Lamphere, Lou
ATTORNEY: Beach, David H.
TITLE OF INVENTION: INHIBITORS OF CELL CYCLE PROGRESSION AND
TITLE OF INVENTION: RELATED THERETO
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:



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OM nucleic - nucleic search, using sw model

Run on: August 29, 2003, 14:10:31 : Search time 1661 seconds
(without alignments)
7796.761 Million cell updates/sec

Title: US-09-865-018b-1

Perfect score: 597
Sequence: 1 atgtcaacgctgcgagctgc... :tggagagagcttcagagcttca 597

Scoring table: IDENTITY_NUC
Gapop 10.0 : Gapext 1.0

Searched: 2278192 seqs, 1152238056 residues

Total number of hits satisfying chosen parameters 45662784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:
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2: em_esthum:
3: em_estlin:
4: em_estmu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_hic:
9: qb_est1:
10: qb_est2:
11: qb_hic:
12: qb_est3:
13: qb_est4:
14: qb_est5:
15: em_estum:
16: em_estom:
17: em_gss_hum:
18: em_gss_inv:
19: em_gss_pln:
20: em_gss_vrl:
21: em_gss_fun:
22: em_gss_mam:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rnd:
26: em_gss_phg:
27: em_gss_vrl:
28: qb_gss1:
29: qb_gss2:

Prod No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	582.8	97.6	918	12	B0554135 B0554135
3	582.6	97.5	601	9	A0127449 A0127449
4	579.8	97.1	920	14	BX410337 BX410337

Result No.	Score	Query Match	Length	DB ID	Description
5	546	91.5	563	12	B055406 B055406
6	514.1	86.2	628	12	B0268198 B0268198
7	475.4	79.8	783	9	A0117463 A0117463
8	469.2	78.4	1884	11	AK047669 AK047669
9	469.2	78.6	3081	11	AK046676 AK046676
10	469.2	78.6	3084	11	AK050430 AK050430
11	461.8	77.4	889	13	B039384 B039384
12	452.6	75.8	967	9	A1542415 A1542415
13	434	72.7	551	12	B0874120 B0874120
14	398.8	66.8	574	12	B0939497 B0939497
15	393.8	66.0	468	9	A0706968 A0706968
16	387.8	65.0	496	9	AM140878 AM140878
17	384.6	64.4	514	10	B0363218 B0363218
18	384.2	64.1	1052	13	BX444594 BX444594
19	381.4	63.9	908	13	B0176107 B0176107
20	380.4	63.7	618	14	CB579171 CB579171
21	374.6	62.7	792	13	B0298908 B0298908
22	374.4	62.7	508	9	A1008468 A1008468
23	373.5	62.6	776	13	B0459515 B0459515
24	362	60.6	819	13	B0459234 B0459234
25	360.6	60.1	634	13	EX276984 EX276984
26	334.8	56.1	709	14	BY719859 BY719859
27	329.2	55.1	657	13	EX276990 EX276990
28	322	54.9	393	9	AM114575 AM114575
29	311.8	52.2	710	13	B0257791 B0257791
30	300.2	50.3	878	9	A151962 A151962
31	299	50.1	436	10	B456444 B456444
32	298.9	50.1	540	9	AV748756 AV748756
33	295.6	49.5	417	10	B0554609 B0554609
34	289.6	48.5	401	10	B0294342 B0294342
35	288.8	48.4	748	9	A0118951 A0118951
36	285.2	47.8	663	13	B0229927 B0229927
37	280.2	46.9	821	12	B1756553 B1756553
38	279.8	46.9	792	10	B0178484 B0178484
39	275.2	46.1	510	13	B0278018 B0278018
40	273.4	45.8	696	13	B0380492 B0380492
41	271.6	45.5	669	10	B0645648 B0645648
42	268.8	45.0	761	10	B0372040 B0372040
43	264.6	44.3	941	13	B0544524 B0544524
44	264.4	44.3	638	13	B0477013 B0477013
45	262.9	44.0	342	10	B0815838 B0815838

ALIGNMENTS

RESULT 1
A0121935
LOGOS
DEFINITION
A0121935 MAMMAL Homo sapiens cDNA clone MAMMAL001309.5, mRNA
SEQUENCE
A0121935
VERSION
A0121935.1 GI:10937170
KEYWORDS
EST
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 842)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, A., Watanabe, A., Nakamura, Y., Nagai, T., Sugano, S. and
Isaichi, T.
JOURNAL
JHG human cDNA project
COMMENT
Unpublished
Contact: Takao Isaai
Genomics Laboratory
Hella Research Institute
1532-3 Yama, Kisarazu, Chiba 275-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI Home: <http://www.hri.co.jp>
Research: <http://hri.hi-hyogo.ac.jp>
Research: <http://hri.hi-hyogo.ac.jp> Library construction Department


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LOCUS       MZ68198              578 bp      mRNA          linear     EST 07-MAY-2003
DEFINITION   J196d02.y1 Human insulinoma pancreatic-DNA clone; IMAGE: 2770250
VERSION      57 similar to SW:CDNB_HUMAN P46527 CYCLIN-DEPENDENT KINASE
AUTHORS      INHIBITOR ID ; , mRNA sequence.
ACCESSION    HQ268198.1 GI:20493247
KEYWORDS     EC:
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominoidea; Homo,
1 (bases 1 to 578)
REFERENCE    Melton,D., Brown,J.E., Kenty,G., Permutt,A., Lee,C., Kastner,K.,
Meltsika,I., Scarce,M., Bresnelli,J., Graymoll,G., Clifton,S.,
Hallier,L., Marra,M., Page,D., Wylie,T., Martin,J., Blisstein,A.,
Schmitt,A., Theising,B.B., Rilter,E., Ponko.I., Bennett.T., Carlines
' M., Gibbons.M., McCann,R., Cole,P.R., Tsagarelshvili,R., Williams,T.,
Jackson,Y., And Bowers.Y.,
Endocrine Pancreas Consortium
Unpublished
JOURNAL
COMMENT      Other ESTS : j196d02.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel.: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr T. Ferrer-In vivo mass-selected
phagescript SK- by Dr. H. Inoue DNA sequencing by Washington
University Genome Sequencing Center For information on obtaining a
clone please contact Dr Hiroshi Inoue (hinoue@mcd.wustl.edu)
Seq primer: -40RP from Gdbco
High quality sequence stop: 429.
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                    /cclone_lib="Human Insulinoma"
                    //note="Organ pancreas; Vector: phagescript SK; Site=1
XhoI; Site=2: EcoRI; Constructed with lambda ZAPI system
(Strategene) by Dr. J. Ferrer, in vivo mass-excised to
paluescript sk- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/rest/lambda_protocol.shtml).
Please Contact Hiroshi Inoue, MD/PhD for further
Information or this library (mdmelton@cbl.washu.edu; Femailty
Laboratory, Washington University School of Medicine, Box
812f, 660 S Euclid Ave., St Louis, MO 63110) Note: This
is a Washington University Pancreas EST project library."
BASE COUNT        151 a         152 c         188 g           87 t
ORIGIN
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DB      183 TTAATCGTAGGATTTGAGAAAGATATGTAAGATATGTAAGATATGTAAGATATGTAAGATATGTA 242
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[illegible]

7. The Board shall have the right to suspend or terminate the membership of any member who fails to pay the dues or assessments or who is found to be in violation of the bylaws or rules of the organization.

